

Amendment to the Claims:

Please amend the claims as follows.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A method for identifying a molecule that modulates transcription the biological activity of a native quadruplex DNA, which comprises comprising

(a) providing a quadruplex DNA; and, a candidate quadruplex DNA-binding molecule, wherein the quadruplex DNA comprises the nucleotide sequence (GGA)<sub>4</sub> (SEQ ID NO:1) or the nucleotide sequence (GGA)<sub>3</sub>GG (SEQ ID NO:2), and G is guanine and A is adenine, and the quadruplex DNA is in a heptad/tetrad conformation;

(b) contacting the a test quadruplex DNA with the [[a]] candidate quadruplex DNA-binding molecule, wherein the test quadruplex DNA comprises the nucleotide sequence (GGA)<sub>4</sub> (SEQ ID NO:1) or the nucleotide sequence (GGA)<sub>3</sub>GG (SEQ ID NO:2), and wherein G is guanine and A is adenine; and

(c) determining the presence or absence of an interaction between the candidate quadruplex DNA-binding molecule and the [[test]] quadruplex DNA, whereby the candidate molecule that interacts with the [[test]] quadruplex DNA is identified as a [[the]] molecule that modulates the transcription the biological activity of the native quadruplex DNA.

Claim 2 (previously presented): The method of claim 1, wherein the [[test]] quadruplex DNA comprises a nucleotide sequence selected from the group consisting of

(GGA)<sub>4</sub>AGA(GGA)<sub>3</sub>GGC (SEQ ID NO:15);

(GGA)<sub>4</sub> (SEQ ID NO:1);

AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16);

GGAGGGGGAGGGG (SEQ ID NO:17);

AGGAGAA(GGA)<sub>2</sub>GGT(GGA)<sub>3</sub>G<sub>3</sub> (SEQ ID NO:18);

(GGA)<sub>3</sub>AGAATGCGA(GGA)<sub>2</sub>G<sub>3</sub>AGGAG (SEQ ID NO:19);

CCGAA(GGA)<sub>2</sub>A(GGA)<sub>3</sub>G<sub>4</sub> (SEQ ID NO:20);

(GGA)<sub>2</sub>CCGA(GGA)<sub>2</sub> (SEQ ID NO:25);

GGAA(GGA)<sub>3</sub> (SEQ ID NO:23);  
AGAAGAG(GGA)<sub>3</sub>G (SEQ ID NO:22); [[and]]  
AGCGA(GGA)<sub>8</sub>GAGGAA (SEQ ID NO:21);  
or a combination thereof.

Claim 3 (currently amended): The method of claim 1, wherein the [[test]] quadruplex DNA comprises a ~~nucleotide sequence that is identical to a nucleotide sequence in native quadruplex DNA sequence.~~

Claim 4 (currently amended): The method of claim 1, wherein the [[test]] quadruplex DNA comprises a ~~nucleotide sequence that is identical to a gene transcription regulatory nucleotide sequence in native quadruplex DNA.~~

Claim 5 (previously presented): The method of claim 4 [[1]], wherein the [[test]] quadruplex DNA comprises a gene transcription regulatory nucleotide sequence found in native quadruplex DNA is in a heptad/tetrad conformation.

Claim 6 (currently amended): The method of claim 1 [[5]], wherein the heptad/tetrad conformation of the [[test]] quadruplex DNA is formed by incubating the quadruplex DNA in a solution comprising potassium ions for a time period less than the time period required to form another quadruplex conformation.

Claim 7 (currently amended): The method of claim 1 [[5]], wherein the [[test]] quadruplex DNA comprises a mutation that hinders formation of another quadruplex conformation.

Claim 8 (currently amended): The method of claim 1, wherein the [[test]] quadruplex DNA is coupled to a reporter expression system.

Claim 9 (original): The method of claim 8, wherein the reporter expression system comprises a luciferase reporter.

Claim 10 (currently amended): The method of claim 1, wherein the presence or absence of an interaction is assayed by a Taq polymerase arrest assay.

Claim 11 (original): The method of claim 1, wherein the interaction is a binding interaction.

Claim 12 (currently amended): A method for modulating ~~the biological activity of a biologically significant native quadruplex DNA transcription, which comprises comprising~~

(a) providing a system comprising quadruplex DNA; and, a quadruplex DNA-binding molecule,

wherein the quadruplex DNA comprises a nucleotide sequence (GGA)<sub>4</sub> (SEQ ID NO:1), a nucleotide sequence (GGA)<sub>3</sub>GG (SEQ ID NO:2), or a combination thereof, and G is guanine and A is adenine, and the quadruplex DNA is in a heptad/tetrad conformation; and

(b) contacting the [[a]] system comprising the native quadruplex DNA with the [[a]] quadruplex DNA-binding molecule that interacts with quadruplex DNA comprising the nucleotide sequence (GGA)<sub>4</sub> (SEQ ID NO:1) or the nucleotide sequence (GGA)<sub>3</sub>GG (SEQ ID NO:2), wherein G is guanine and A is adenine; whereby the molecule modulates the biological activity of a biologically significant native quadruplex DNA thereby modulating transcription.

Claim 13 (currently amended): The method of claim 12, wherein the native quadruplex DNA comprises a nucleotide sequence selected from the group consisting of (GGA)<sub>4</sub>AGA(GGA)<sub>3</sub>GGC (SEQ ID NO:15); (GGA)<sub>4</sub> (SEQ ID NO:1); AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16); GGAGGGGGAGGGG (SEQ ID NO:17); AGGAGAA(GGA)<sub>2</sub>GGT(GGA)<sub>3</sub>G<sub>3</sub> (SEQ ID NO:18); (GGA)<sub>3</sub>AGAATGCGA(GGA)<sub>2</sub>G<sub>3</sub>AGGAG (SEQ ID NO:19);

CCGAA(GGA)<sub>2</sub>A(GGA)<sub>3</sub>G<sub>4</sub> (SEQ ID NO:20);  
(GGA)<sub>2</sub>CCGA(GGA)<sub>2</sub> (SEQ ID NO:25);  
GGAA(GGA)<sub>3</sub> (SEQ ID NO:23);  
AGAAGAG(GGA)<sub>3</sub>G (SEQ ID NO:22); [[and]]  
AGCGA(GGA)<sub>8</sub>GAGGAA (SEQ ID NO:21);  
or a combination thereof.

Claim 14 (currently amended): The method of claim 12, wherein the [[test]] quadruplex DNA is in a native heptad/tetrad conformation.

Claim 15 (currently amended): The method of claim 12 [[14]], wherein the heptad/tetrad conformation of the [[test]] quadruplex DNA is formed by incubating the DNA in a solution comprising potassium ions for a time period less than the time period required to form another quadruplex conformation.

Claim 16 (currently amended): The method of claim 12 [[14]], wherein the [[test]] quadruplex DNA comprises a mutation that hinders formation of another quadruplex conformation.

Claim 17 (original): The method of claim 12, wherein the system is a cell.

Claim 18 (original): The method of claim 12, wherein the system is an organism.

Claim 19 (currently amended): A method for identifying the presence or absence of a quadruplex structure in a nucleic acid of a sample, which comprises comprising  
(a) providing a sample comprising a nucleic acid; and, a quadruplex-interacting agent,  
wherein the quadruplex-interacting agent binds to a quadruplex structure in a heptad/tetrad  
conformation;

(b) contacting the sample with the [[a]] quadruplex-interacting agent; and

(c) detecting the presence or absence of an interaction between the nucleic acid quadruplex structure and the quadruplex-interacting agent, whereby the presence of an interaction is indicative the presence of the quadruplex structure in the nucleic acid.

Claim 20 (currently amended): The method of claim 19, wherein the quadruplex-interacting agent comprises [[is]] TMPyP4 or telomestatin.

Claim 21 (currently amended): The method of claim 19, wherein the quadruplex-interacting agent binds to the quadruplex structure [[is]] in a native heptad/tetrad conformation.

Claim 22 (previously presented): A method for identifying a nucleotide sequence capable of forming a quadruplex structure, which comprises identifying in a database a subset of nucleotide sequences comprising (GGA)<sub>4</sub> (SEQ ID NO:1), (GGA)<sub>3</sub>GG (SEQ ID NO:2) or (GGA)<sub>3</sub>GGX<sub>n</sub>(GGA)<sub>3</sub>GG, wherein n is an integer between 0 and 3 (SEQ ID NOS:3-6).

Claim 23 (original): The method of claim 22, which further comprises identifying nucleotide sequences from the subset of nucleotide sequences adjacent to a gene coding region.

Claim 24 (original): The method of claim 22, which further comprises identifying nucleotide sequences from the subset of nucleotide sequences identical to or substantially identical to an oncogene nucleotide sequence.

Claim 25 (currently amended): A method for identifying a nucleotide sequence capable of forming a quadruplex structure, which comprises contacting a cell with a quadruplex interacting agent, identifying a subset of RNA nucleotide sequences increased or decreased 2-fold or [[of]] more in the cell as compared to a cell not contacted with the quadruplex interacting agent, and identifying a nucleotide sequence from the subset comprising (GGA)<sub>4</sub> (SEQ ID NO:1), (GGA)<sub>3</sub>GG (SEQ ID NO:2) or (GGA)<sub>3</sub>GGX<sub>n</sub>(GGA)<sub>3</sub>GG (SEQ ID NO:4) as the nucleotide sequence capable of forming a quadruplex structure.

Claim 26 (currently amended): The method of claim 25, wherein the quadruplex interacting agent comprises [[is]] TMPyP4 or telomestatin.

Claim 27 (new): A method for identifying a molecule that modulates the biological activity of a native quadruplex DNA, which comprises

contacting a test quadruplex DNA with a candidate molecule, wherein the test quadruplex DNA comprises the nucleotide sequence AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16), and wherein G is guanine and A is adenine; and determining the presence or absence of an interaction between the candidate molecule and the test quadruplex DNA, whereby the candidate molecule that interacts with the test quadruplex DNA is identified as the molecule that modulates the biological activity of the native quadruplex DNA.

Claim 28 (new): The method of claim 27, wherein the test quadruplex DNA further comprises a nucleotide sequence comprising (GGA)<sub>4</sub>AGA(GGA)<sub>3</sub>GGC (SEQ ID NO:15); (GGA)<sub>4</sub> (SEQ ID NO:1); GGAGGGGGAGGG (SEQ ID NO:17); AGGAGAA(GGA)<sub>2</sub>GGT(GGA)<sub>3</sub>G<sub>3</sub> (SEQ ID NO:18); (GGA)<sub>3</sub>AGAATGCGA(GGA)<sub>2</sub>G<sub>3</sub>AGGAG (SEQ ID NO:19); CCGAA(GGA)<sub>2</sub>A(GGA)<sub>3</sub>G<sub>4</sub> (SEQ ID NO:20); (GGA)<sub>2</sub>CCGA(GGA)<sub>2</sub> (SEQ ID NO:25); GGAA(GGA)<sub>3</sub> (SEQ ID NO:23); AGAAGAG(GGA)<sub>3</sub>G (SEQ ID NO:22); AGCGA(GGA)<sub>8</sub>GAGGAA (SEQ ID NO:21); or a combination thereof.

Claim 29 (new): A method for identifying a nucleotide sequence capable of forming a quadruplex structure, which comprises identifying in a database a subset of nucleotide sequences comprising AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16).

Claim 30 (new): A method for identifying a nucleotide sequence capable of forming a quadruplex structure, which comprises contacting a cell with a quadruplex interacting agent, identifying a subset of RNA nucleotide sequences increased or decreased 2-fold or more in the cell as compared to a cell not contacted with the quadruplex interacting agent, and identifying a

nucleotide sequence from the subset comprising AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16) as the nucleotide sequence capable of forming a quadruplex structure.

Claim 31 (new): A method for identifying the presence or absence of a quadruplex structure in a nucleic acid of a sample, comprising

- (a) providing a sample comprising a nucleic acid comprising AGAGAAGAGG(GGA)<sub>5</sub>GAGGAGGAGGCGC (SEQ ID NO:16); and, a quadruplex-interacting agent, wherein the quadruplex-interacting agent binds to a quadruplex structure in a heptad/tetrad conformation;
- (b) contacting the sample with the quadruplex-interacting agent; and
- (c) detecting the presence or absence of an interaction between the nucleic acid quadruplex structure and the quadruplex-interacting agent, whereby the presence of an interaction is indicative the presence of the quadruplex structure in the nucleic acid.